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cons.aa	G T G V	A K	E
htGFBR-II	LDTLVGKGRFAEVYKAJLKQNTSEQFETVAVKIFFPYDHYASWKRKDIFSDINLICHENILOF		
mActR-II B	LLEIKARGRFGCVWKAQLMN-----DFVAVKIKPLQDKQSWQSERIFSTPGMHENILQF		
mActR-II	LLEVAKARGRFGCVWKAQLLN-----EYVAVKIFFPIQDKQSWQNEYEVYSIPGMHENILOF		
daf-1	LTURVGSGRFGNVSRGODYRG-----EAVAVKVFNAIDEPAFHKEIEIFETRMLRHNPVLRY		
subdomains	I	II	III
			IV

htGFBR-II	LTAEEERKTELKGQYWLITAFHAKGNLQEYLTRHVI SWEDLRNVGSSLARGLSHLHSDDHTP-C		
mActR-II B	IAAEKRGSNLEVELWLITAFHDKGSLIDYLKGNITWNELCHVAETMSRGISYLYEDVPWCR		
mActR-II	IGAEERGTSVDVDLWLITAFHEKGSLSDFLKANVSWNELCHIAETMARGLAYLHEDIPGLK		
daf-1	IGSDRVDTGFVTTELWLVI EYHPSGSLHDFFLENTVNIETYYNLMRSTASGLAFLHNQICGSK		
subdomains	V		VI-A

cons.aa	DLK N	DFG
htGFBR-II	-GRPEMPIVHRDLKSSNIVKNDLTCCLCDPGLSLRL---GPySSVDDLANSQVGTARYMAP	
mActR-II B	GEGHKPSIAHRDFKSKNVLLKSDLTAVLADPGLA VRF---EPGKPPGD--THGQVGTRRYMAP	
mActR-II	-DGHKPAI SHRDIIKSKNVLLQNLTACIADPGLALKF---EACKSAGD--THGQVGTRRYMAP	
daf-1	-ESNKPMAMHRDIKSNTIMYQNDLTCAIGDLGLSLSKPEDAASDIIAN--ENYKCGTVRYLAP	
subdomains	VI-B	VII
		VIII

Fig. 1

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a.a C C E G N M C  
5' GCGGATCCTGTTGTGAAGGNAATATGTG 3' Fig. 2A  
BamHI C C G C

a.a V A V K I F  
5' GCGGATCCGTCGCAGTCAAAATTT 3' Fig. 2B  
BamHI G C G G C  
T T T A

a.a R D I K S K N  
5' GCGGATCCCGATATTAAAAGCAA 3' Fig. 2C  
BamHI A C C GTCT  
G A

a.a E P A M Y  
5' CGGAATTCTGGTGCCATATA Fig. 2D  
EcoRI G G G  
A A

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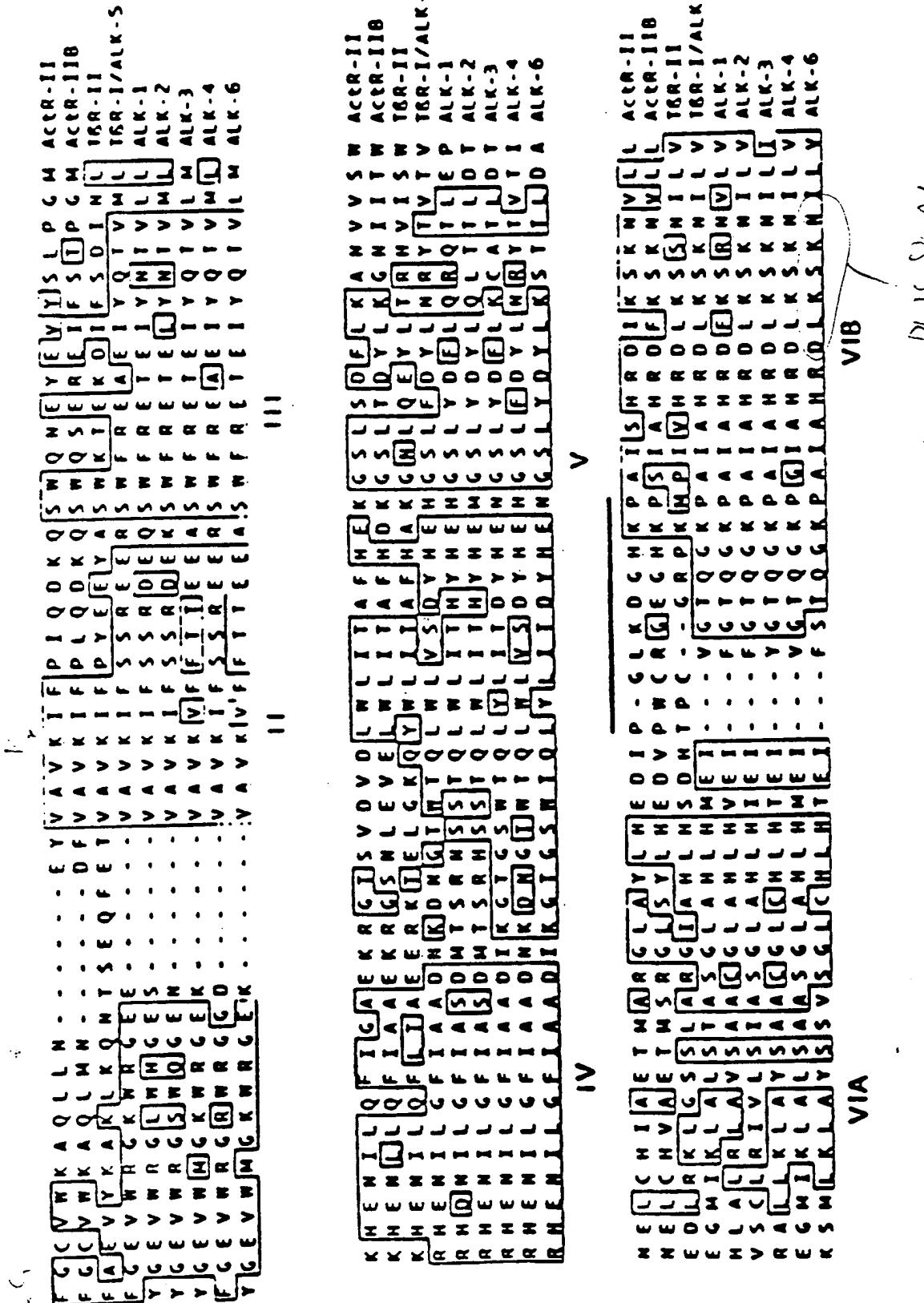
ACTR-11  
 ACTR-116  
 TBR-11  
 TBR-11/ALK-5  
 ALK-1  
 ALK-2  
 ALK-3  
 ALK-4  
 ALK-5  
 ALK-6

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Y ACCR-11  
Y ACCR-118  
Y TCR-11  
Y TCR-11ALK-S  
Y ALK-1  
Y ALK-2  
Y ALK-3  
Y ALK-4  
Y ALK-6

Fig. 3 contd.



0 2 0 3 3 1 2 2 0 2 1 1 5 3

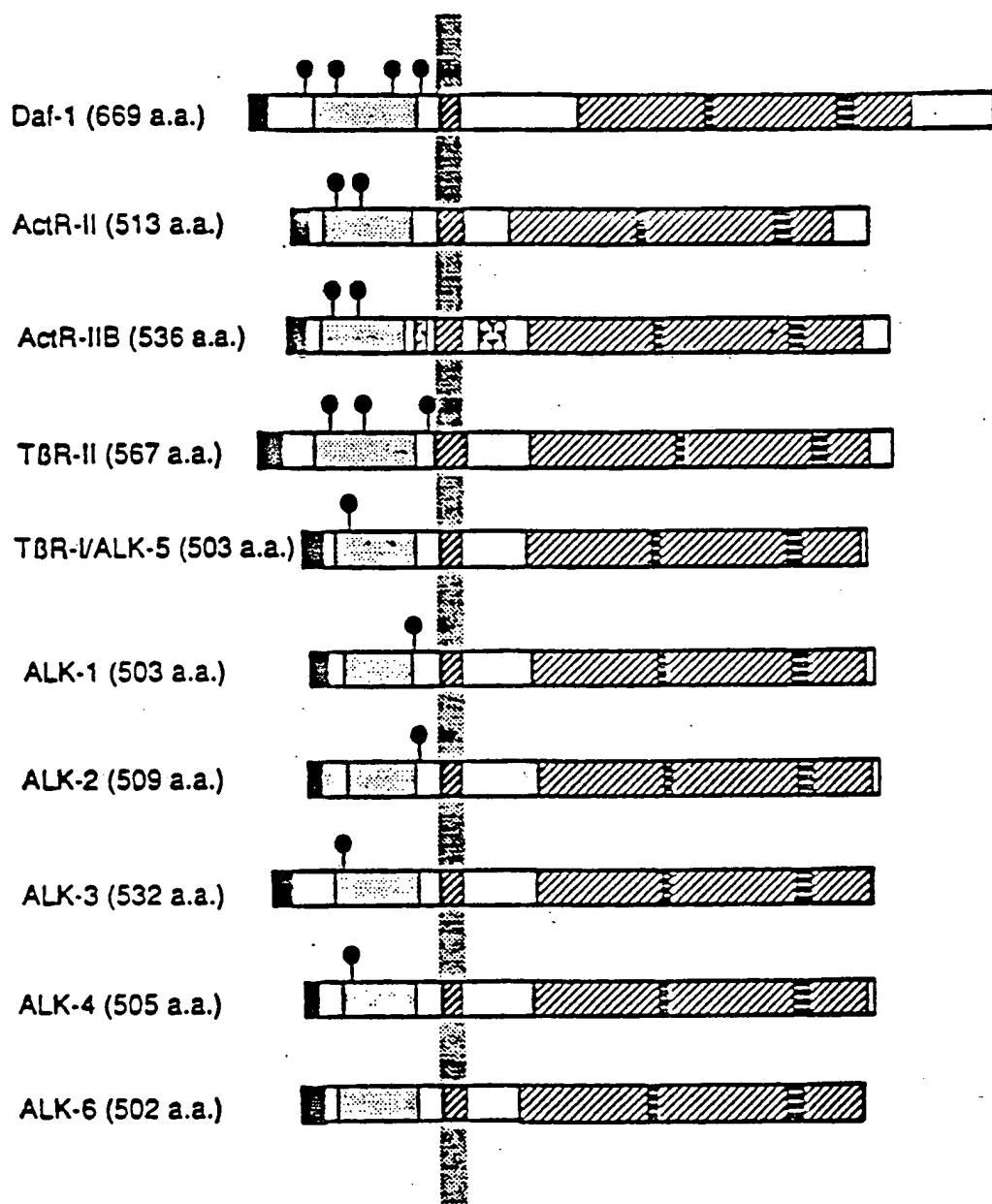
VIII (16. 1. 17)

ACCR-11  
ACCR-116  
TBR-11  
ALK-1  
ALK-2  
ALK-3  
ALK-4  
ALK-5  
ALK-6

XIX

Fig. 3 contd.

Fig. 3 contd.



█	signal sequence	█	insert in the kinase domain
▨	cysteine-rich region	●	potential N-glycosylation site
▨	transmembrane domain	▨	alternatively spliced region
▨▨	serine/threonine kinase domain		

Fig. 4

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C - F	- - - - -	C X G D - D I - - T C E T - - G - C F V S L - - S D C Majority	
C - T	- - - - -	G E S P - - - - -	ALK-1/CR
C - C	- - - - -	H C K G P - - - - -	ALK-2/CR
C - Y	- - - - -	H C E G L - - - - -	ALK-3/CR
C - A	- - - - -	H C S G - - - - -	ALK-4/CR
C - F	- - - - -	H C T S - - - - -	ALK-5/CR
CLEFN	- - - - -	H C H L - - - - -	ActR-11/CR
CLEYN	- - - - -	H C N E K D R T N O T G V E P C Y G D K D K R R H C Y A S - - - - -	ActR-11B/CR
CKE	- - - - -	H C D N Q K S C H S N C S I T S I C E K P Q E V C Y A V M R K N D E	TOR-11/CR
CHCSREV	- - - - -	H C F L N E T D R S F Y E N T - - - - -	DAF-1/CR
Majority		Majority	
I E I V E K G C - - - - -	C Y D R T L - - - - -	G S P F - C V K S P K S P G - T V T E C - C E G D L C	
R H P Q E H R C - - - - -	G C N L H - - - - -	R E L - G R C R P T E - F V N H Y C - C D S H L C	ALK-1/CR
F H V Y O K G C - - - - -	F O V Y - - - - -	O G K M T C - K I P P S P G O A Y - E C - C O G D M C	ALK-2/CR
G E T T L A S C - - - - -	F H K Y E - - - - -	G S D F Q C K D S P R A O L R N T H C - C R P T N L C	ALK-3/CR
M E H H V R T C - - - - -	I P K V E L Y P A G K P F Y C L S S E D - - - L R N T H C - C Y T D Y C	ALK-4/CR	
K V T H N S M C - - - - -	I A E I D L I P R D R P E - - - V C A P S S K T C S V T T Y C - C N Q D H C	ALK-5/CR	
I E I V K Q G C H L D D I N C Y D R T D - - - - -	C V E K K D S P E - - - V Y F C C C E G N H C	ActR-11/CR	
I E I V K K C H D P K L P Y H D F I T E D A A S P K C I M K E K K K D P H A T Y W I C C D K G N F C	C Y A T E N P Q - - - V Y F C C C E G N F C	ActR-11B/CR	
N I T T L E T Y C H D P K L P Y H D F I T E D A A S P K C I M K E K K K D P H A T Y W I C C D K G N F C	T F F M C S C S S D E C	TOR-11/CR	
P E I S H F G C - - - - -	V T D E I T E F H D T A K V G C - - - R P S D E C	DAF-1/CR	

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ALK-2	ALK-3	ALK-4	ALK-5	ActR-II	ActR-IIB	TBR-II	daf-1	
79	60	61	63	40	40	37	39	ALK-1
	63	64	65	41	39	37	39	ALK-2
	63	65	41	38	37	39		ALK-3
		90	41	40	39	42		ALK-4
			42	40	41	43		ALK-5
				78	48	35		ActR-II
					47	32		ActR-IIB
						34		TBR-II

Fig. 6

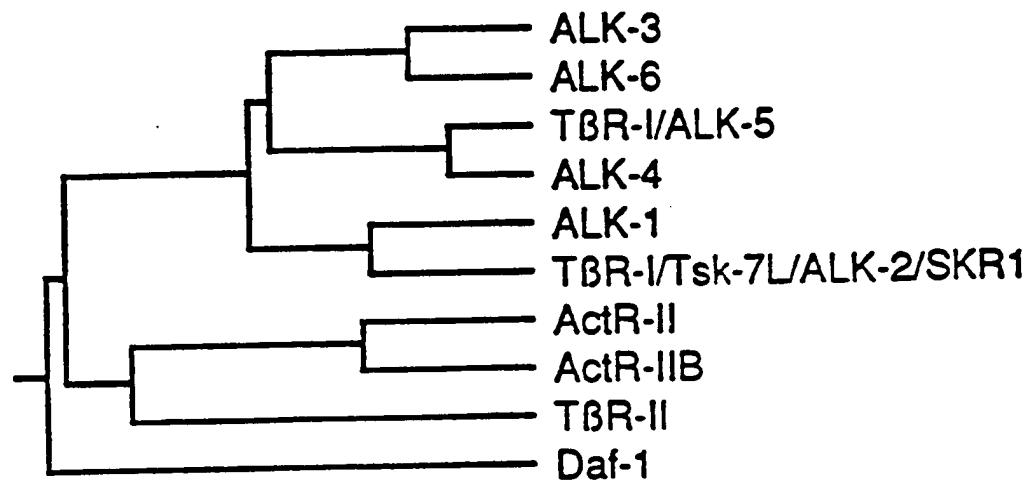


Fig. 7